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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/445,614A

DATE: 04/16/2002

TIME: 11:30:33

#15

Input Set : A:\T1481\SL.TXT

Output Set: N:\CRF3\04162002\I445614A.raw

ENTERED

4 <110> APPLICANT: Bonnert, Timothy Peter
 6 <120> TITLE OF INVENTION: HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR
 9 <130> FILE REFERENCE: T1481
 11 <140> CURRENT APPLICATION NUMBER: 09/445,614A
 12 <141> CURRENT FILING DATE: 1999-12-08
 14 <150> PRIOR APPLICATION NUMBER: 9827016.8
 15 <151> PRIOR FILING DATE: 1998-12-08
 17 <160> NUMBER OF SEQ ID NOS: 19
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2469
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <400> SEQUENCE: 1

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28 ggtcctggct ggaccgagca gcctccctcct ccttagatga cctcacccctc cagctctcca	120
29 gtttcaggt tggagacatt agatggaggc caagaagatg gctctgaggc ggacagagga	180
30 aagctggatt ttgggagcgg gtcgcctccc atggagtac agttccaggcg cgaggaccgg	240
31 aaattcgccc ctcagataag agtcaacctc aactaccgaa agggAACAGG tgccagtca	300
32 ccggatccaa accgatttga ccgagatcgg ctcttcaatg cggctctcccg gggtgtcccc	360
33 gaggatctgg ctggacttcc agagtaacctg agcaagacca gcaagtacat caccgactcg	420
34 gaatacacag agggctccac aggttaagacg tgcctgatga aggctgtgtc gAACCTTAAG	480
35 gacggagtca atgcctgcat tctgccactg ctgcagatcg acaggagactc tggcaatcct	540
36 cagcccctgg taaatgcccgt gtgcacagat gactattacc gaggccacag cgctctgcac	600
37 atcgccattt agaagaggag tctgcagtgt gtgaagctcc tgggtggagaa tggggccaat	660
38 gtgcattgccc gggcctgccc cgccttcttc cagaaggccc aaggacttg cttttatttc	720
39 ggtgagctac ccctctctt ggccgcttgc accaaggcgt gggatgtgtt aagctacctc	780
40 ctggagaacc cacaccagcc cgccagcctg caggccactg actcccaggc caacacagtc	840
41 ctgcattgccc tagtgatgtat ctggacaac tcagctgaga acattgcact ggtgaccagc	900
42 atgtatgtat ggctccctca agctggggcc cgcctctgccc ctaccgtgca gcttgaggac	960
43 atccgcaacc tgcaggatct cacgcctctg aagctggccg ccaaggaggg caagatcgag	1020
44 atttcaggc acatccgtca gcgaggatctt tcaggactga gccacatttc ccgaaaggttc	1080
45 accgagtggc gctatggcc tggccgggtc tcgcgtatgc acctggcttc tgtgacagc	1140
46 tgtgaggaga actcagtgtc ggagatcatt gccttccatt gcaagagccc gcaccgacac	1200
47 cgaatggcgtc tttggagcc ctogaacaaa ctgcgtcagg cggaaatggga tctgtctatc	1260
48 cccaaattct tcttaaactt ctgtgttaat ctgatctaca tggatctttt caccgctgtt	1320
49 gcttaccatc agcctaccct gaagaagcag gcccgcctc acctgaaagc ggaggttgaa	1380
50 aactccatgc tgctgacggg coacatccctt atcctgttag gggggatcta cctccctcggt	1440
51 ggccagctgt ggtacttctg gcccgcctc gtgttcatct ggtatctcggtt catagacagc	1500
52 tacatttggaaa tccctcttccctt gttccaggcc ctgcctcacag tgggtgtccca ggtgtgtgt	1560
53 tccctggcca tcgagttggta ctgccttccctg cttgtgtctg cgctgggtgt gggctggctg	1620
54 aacctgctttt actatacacg tggcttccag cacacaggca tctacagtgt catgtatccag	1680
55 aaggtcatcc tgcgggaccc gtcgcgttcc ctgtatctt acttagtctt cctttccgc	1740

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56	ttcgctgttag	ccctggtag	cctgagccag	gaggottggc	gcccccgaagc	tcctacaggc	1800
57	cccaatgcca	cagagtca	gcagccatg	gagggacagg	aggacgaggg	caacggggcc	1860
58	cagtaggg	gtatccatg	agcccttgc	gagctttca	aattcacat	cgcatgggc	1920
59	gagetggct	tccaggagca	gtgcacttc	cgcggatgg	tgctgctgt	gctgctggcc	1980
60	tacggtctgc	tcacctacat	cctgctgctc	aacatgtca	tcgcccctcat	gagcgagacc	2040
61	gtcaaacatgt	tcgcccactga	cagctggagc	atctgaaagc	tgcagaaaagc	catctctgtc	2100
62	ctggagatgg	agaatggcta	ttgggtgtgc	aggaagaagc	agcgggcagg	tgtgtatgtc	2160
63	accgttggca	ctaagccaga	tggcagcccg	gatgagcgct	gtgtgttcag	ggtggaggag	2220
64	gtgaactggg	cttcatggg	gcagacgctg	cctacgtgt	gtgaggacc	gtcagggggca	2280
65	ggtgtccctc	gaactctcg	gaaccctgtc	ctggcttccc	ctccccaaagg	ggatgaggat	2340
66	ggtgcctctg	aggaaaacta	tgtgcccgtc	cagctctcc	agtccaaactg	atggcccaga	2400
67	tgcagcagga	ggccagagga	cagagcagag	gatcttcca	accacatctg	ctggctctgg	2460
68	ggtcccagt						2469

70 <210> SEQ ID NO: 2

71 <211> LENGTH: 824

72 <212> TYPE: PRT

73 <213> ORGANISM: Homo sapiens

75 <400> SEQUENCE: 2

76	Met	Thr	Ser	Pro	Ser	Ser	Pro	Val	Phe	Arg	Leu	Glu	Thr	Leu	Asp		
77	1				5				10				15				
78	Gly	Gly	Gln	Glu	Asp	Gly	Ser	Glu	Ala	Asp	Arg	Gly	Lys	Leu	Asp	Phe	
79							20			25			30				
80	Gly	Ser	Gly	Leu	Pro	Pro	Met	Glu	Ser	Gln	Phe	Gln	Gly	Glu	Asp	Arg	
81							35			40			45				
82	Lys	Phe	Ala	Pro	Gln	Ile	Arg	Val	Asn	Leu	Asn	Tyr	Arg	Lys	Gly	Thr	
83							50			55			60				
84	Gly	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe	
85							65			70			75				
86	Asn	Asn	Ala	Val	Ser	Arg	Gly	Val	Pro	Gly	Ala	Gly	Gly	Ala	Thr	Cys	Thr
87							85			90			95				
88	Gly	Gly	Cys	Thr	Gly	Gly	Ala	Cys	Thr	Thr	Cys	Cys	Ala	Gly	Ala	Gly	
89							100			105			110				
90	Thr	Ala	Cys	Cys	Thr	Gly	Ala	Gly	Cys	Ala	Ala	Gly	Ala	Cys	Cys	Ala	
91							115			120			125				
92	Gly	Cys	Ala	Ala	Gly	Thr	Ala	Cys	Cys	Thr	Cys	Ala	Cys	Cys	Gly	Ala	
93							130			135			140				
94	Cys	Thr	Cys	Gly	Glu	Asp	Leu	Ala	Gly	Leu	Pro	Glu	Tyr	Leu	Ser	Lys	
95							145			150			155				
96	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu	Gly	Ser	Thr	Gly	
97							165			170			175				
98	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Leu	Asn	Leu	Lys	Asp	Gly	Val	Asn	
99							180			185			190				
100	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp	Ser	Gly	Asn	Pro	
101							195			200			205				
102	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr	Tyr	Arg	Gly	His	
103							210			215			220				
104	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu	Gln	Cys	Val	Lys	
105							225			230			235				
106	Leu	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg	Ala	Cys	Gly	Arg

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107	245	250	255
108	Phe Phe Gln Lys Gly Gln Gly Thr Cys Phe Tyr Phe Gly Glu Leu Pro		
109	260	265	270
110	Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val Val Ser Tyr Leu		
111	275	280	285
112	Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala Thr Asp Ser Gln		
113	290	295	300
114	Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser Asp Asn Ser Ala		
115	305	310	315
116	Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly Leu Leu Gln Ala		
117	325	330	335
118	Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp Ile Arg Asn Leu		
119	340	345	350
120	Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu Gly Lys Ile Glu		
121	355	360	365
122	Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly Leu Ser His Leu		
123	370	375	380
124	Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val Arg Val Ser Leu		
125	385	390	395
126	Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn Ser Val Leu Glu		
127	405	410	415
128	Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His Arg Met Val Val		
129	420	425	430
130	Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp Asp Leu Leu Ile		
131	435	440	445
132	Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile Tyr Met Phe Ile		
133	450	455	460
134	Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys Lys Gln Ala Ala		
135	465	470	475
136	480		
137	Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu Leu Thr Gly His		
138	485	490	495
139	Ile Leu Ile Leu Gly Gly Ile Tyr Leu Leu Val Gly Gln Leu Trp		
140	500	505	510
141	Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser Phe Ile Asp Ser		
142	515	520	525
143	Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu Thr Val Val Ser		
144	530	535	540
145	Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu Pro Leu Leu Val		
146	545	550	555
147	560		
148	Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr Tyr Thr Arg Gly		
149	565	570	575
150	Ile Leu Ile Tyr Ser Val Met Ile Gln Lys Val Ile Leu		
151	580	585	590
152	Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val Phe Leu Phe Gly		
153	595	600	605
154	Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala Trp Arg Pro Glu		
155	610	615	620
156	Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln Pro Met Glu Gly		
157	625	630	635
158	640		

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156 Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Glu Ala
157           645           650           655
158 Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe
159           660           665           670
160 Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Ala
161           675           680           685
162 Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu
163           690           695           700
164 Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp
165 705           710           715           720
166 Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp
167           725           730           735
168 Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr
169           740           745           750
170 Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu
171           755           760           765
172 Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr Leu Cys Glu Asp
173           770           775           780
174 Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn Pro Val Leu Ala
175 785           790           795           800
176 Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu Glu Asn Tyr Val
177           805           810           815
178 Pro Val Gln Leu Leu Gln Ser Asn
179           820
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 51
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Primer
189 <400> SEQUENCE: 3
190 tggttaccaat ctgaagtggg agcggccgcc tcatttttt tttttttttt t      51
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 21
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: PCR Primer
200 <400> SEQUENCE: 4
201 caggccccggg catgcacatt g      21
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 21
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: PCR Primer
211 <400> SEQUENCE: 5
212 ccagggcgag gaccggaaat t      21
214 <210> SEQ ID NO: 6

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215 <211> LENGTH: 21
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: PCR Primer
222 <400> SEQUENCE: 6
223 gacagctgga gcatctggaa g 21
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 21
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: PCR Primer
233 <400> SEQUENCE: 7
234 gacagctgga gcatctggaa g 21
236 <210> SEQ ID NO: 8
237 <211> LENGTH: 21
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: PCR Primer
244 <400> SEQUENCE: 8
245 cttccagatg ctccagctgt c 21
247 <210> SEQ ID NO: 9
248 <211> LENGTH: 21
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Primer
255 <400> SEQUENCE: 9
256 tttgccacca gaattcactg g 21
258 <210> SEQ ID NO: 10
259 <211> LENGTH: 21
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: PCR Primer
266 <400> SEQUENCE: 10
267 ctctcttgg ccgcctgcac c 21
269 <210> SEQ ID NO: 11
270 <211> LENGTH: 21
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: PCR Primer
277 <400> SEQUENCE: 11
278 ccagcactga gttctcctca c 21
280 <210> SEQ ID NO: 12
281 <211> LENGTH: 21

VERIFICATION SUMMARY
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